## SEQUENCE LISTING

- <110> Sim, Gek-Kee Yang, Shumin Sellins, Karen S.
- <120> NOVEL FORMS OF T CELL COSTIMULATORY PROTEINS, NUCLEIC
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- <130> IM-1-C1-PCT
- <140> not yet assigned
- <141> 1999-03-19
- <150> 60/078,765
- <151> 1998-03-19
- <150> 09/062,597
- <151> 1998-04-17
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Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg 85 90 95

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Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Leu Val Lys Thr 165 170 175

Glu Asn Ser Ser Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 180 185 190

Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Ser Phe Ser Val 195 200 205

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<211> 987

<212> DNA

<213> Canis familiaris

<400> 10

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987

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		cac His				_	_				_			_	-	159
		tac Tyr 30		_												207
_	_	gca Ala	_	_		-										255
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	-	gac Asp										_	_	-	_	399
-		gac Asp 110										-				447

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a <sup>-</sup>																1024

<210> 12

<211> 235

<212> PRT

<213> Canis familiaris

<400> 12

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- Ser Cys Asp Tyr Asn Ile Ser Thr Thr Glu Leu Met Lys Val Arg Ile 50 55 60
- Tyr Trp Gln Lys Asp Asp Glu Val Val Leu Ala Val Thr Ser Gly Gln 65 70 .75 80
- Thr Lys Val Trp Ser Lys Tyr Glu Asn Arg Thr Phe Ala Asp Phe Thr . 85 90 95
- Asn Asn Leu Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
  100 105 110
- Lys Tyr Thr Cys Ile Val Gln Lys Thr Glu Lys Arg Ser Tyr Lys Val
- Lys His Met Thr Ser Val Met Leu Leu Val Arg Ala Asp Phe Pro Val 130 135 140
- Pro Ser Ile Thr Asp Leu Gly Asn Pro Ser His Asp Ile Lys Arg Ile 145 150 155 160
- Met Cys Ser Thr Ser Gly Gly Phe Pro Lys Pro His Leu Ser Trp Trp 165 170 175 .
- Glu Asn Glu Glu Glu Leu Asn Ala Ala Asn Thr Thr Val Ser Gln Asp 180 185 190
- Pro Asp Thr Glu Leu Tyr Thr Ile Ser Ser Glu Leu Asp Phe Asn Ile
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- Thr Ser Asn His Ser Phe Val Cys Leu Val Lys Tyr Gly Asp Leu Thr 210 215 220
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<210> 13

<211> 1024

<212> DNA

<213> Canis familiaris

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<210> 14

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<212> DNA

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acagtgaaag aagtagcagt actgtcctgt gattacaaca tttccactac agaactgatg 180
aaagttcgaa tctattggca aaaggatgat gaagtggtgc tggctgtcac atctggacaa 240
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<210> 15

<211> 705

<212> DNA

<213> Canis familiaris

<400> 15

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	> CD	s														
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Val 15	Met	Thr	Leu	Leu	Leu 20	Tyr	Gly	Ala	Ala	Ser 25	Met	ŗàs	Ser	Gin	Ala 30	
		aac	_			-	_		-							144
Tyr	Phe	Asn	Lys	Thr 35	Gly	Glu	Leu	Pro	Cys 40	His	Phe	Thr	Asn	Ser 45	Gln	
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Asn	Ile	Ser	Leu 50	Asp	Glu	Leu	Val	Val 55	Phe	Trp	Gln	Asp	Gln 60	Asp	Lys	
ctg	gtt	ctg	tac	gag	cta	tac	aga	ggc	aaa	gag	aac	cct	caa	aat	gtt	240
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Leu 95	Arg	Leu	His	Asn	Ile 100	Gln	Ile	Lys	Asp	Lys 105	Gly	Leu	Tyr	Gln	Cys 110	
	_	cat													-	384
Phe	Val	His	His	Lys 115	Gly	Pro	Lys	Gly	Leu 120	Val	Pro	Met	His	Gln 125	Met	
aat	tct	gac	cta	tca	gtg	ctt	gct	aac	ttc	agt	caa	cct	gaa	ata	atg	432
Asn	Ser	Asp	Leu	Ser	Val	Leu	Ala	Asn	Phe	Ser	Gln	Pro	Glu	Ile	Met	

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		=		tat ttt ttg gt. Tyr Phe Leu Va.	
				atg aag aaa tc Met Lys Lys Se 19	r
	_			agc ttg tcc tt Ser Leu Ser Ph 205	
				gtc ctg caa ct Val Leu Gln Le 220	
	Lys Leu Pro		Tyr Asn Ile	gaa acc aac aa Glu Thr Asn Ly 235	
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-	gac aac agt Asp Asn Ser 275			aga gtaaagtcca	866
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<210> 17

<211> 280

<212> PRT

<213> Canis familiaris

<400> 17

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Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Glm Asn Ile
35 40 45

Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu Val
50 55 60

Leu Tyr Glu Leu Tyr Arg Gly Lys Glu Asn Pro Gln Asn Val His Arg
65 70 75 80

Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu Arg 85 90 95

Leu His Asn Ile Gln Ile Lys Asp Lys Gly Leu Tyr Gln Cys Phe Val

100 105 110

His His Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Asn Ser 115 120 125

Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Met Val Thr 130 135 140

Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser Ser 145 150 155 160

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Leu Val Lys Thr 165 170 175

Glu Asn Ser Ser Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 180 185 190

Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Ser Phe Ser Val 195 200 205

Pro Glu Ala Ser Asn Val Ser Ile Phe Cys Val Leu Gln Leu Glu Ser 210 215 220

Met Lys Leu Pro Ser Leu Pro Tyr Asn Ile Glu Thr Asn Lys Val Glu 225 230 235 240

Arg Lys Glu Ser Glu Gln Thr Lys Glu Arg Val Arg Tyr His Glu Thr 245 250 255

Glu Arg Ser Asp Glu Ala Gln Cys Val Asn Ile Ser Lys Thr Ala Ser 260 265 270

Gly Asp Asn Ser Thr Thr Gln Phe 275 280

<210> 18

<211> 1795

<212> DNA

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ctccagtctt gttgaaatat gcttgactct tcatggaagc agcaccatag agcaggaggg 1740
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<210> 19

<211> 840

<212> DNA

<213> Canis familiaris

<400> 19

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cagateaagg acaagggett gtateaatgt ttegteate ataaagggee caaaggaete 360
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tetateaget tgteettete agteeetgaa geaageaatg tgageateet etgtgteetg 660
caacttgagt caatgaaget teeeteecta eettataata tagaaaceaa caaagtggag 720
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gaageecagt gtgttaacat ttegaagaea getteaggeg acaacagtae tacacagttt 840

<sup>&</sup>lt;210> 20

<sup>&</sup>lt;211> 840

<sup>&</sup>lt;212> DNA

<sup>&</sup>lt;213> Canis familiaris

<sup>&</sup>lt;400> 20

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<210> 21

<211> 18

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic
Primer

<400> 21

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18

<210> 22

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic Primer <400> 22 22 gtagaaactc ctcagaacaa tg <210> 23 <211> 19 <212> DNA <213> Artificial Sequence <220> <223> Description of Artificial Sequence: Synthetic Primer <400> 23 gtagtatttt ggcaggacc 19 <210> 24 <211> 23 <212> DNA <213> Canis familiaris <400> 24 23 tagaygsgca ggtcaaattt atg <210> 25 <211> 2830 <212> DNA <213> Felis catus <220> <221> CDS <222> (179)..(1174) <400> 25 gtttttttt ttttgagttc tagtctcagc cctgacatta tttctttctc tacaaagagt 60 gttaggaagt tatggggagc tcacaaaggc tcctcatcgt ttattcttaa caccttgttt 120 ctgtgttcct cgggaatgtc actgagctta tacatctggt ctctgggagc tgcagtgg atg ggc att tgt gac agc act atg gga ctg agt cac act ctc ctt gtg 226 Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val 1 15

-	-	ctc Leu	_				-		_	_	-		_		274
		aag Lys 35			_	-									322
	_	ctg Leu	_		_	_	_		 	_	_	-	_	_	370
_	_	tat Tyr													418
		tat Tyr	-	-											466
-		cac His		-											514
		tat Tyr 115													562
		cta Leu													610
	Ser	aat Asn	_												658
		caa Gln													706
		aat Asn		Thr		-									754
		gtg Val 195	Thr					Val				Pro			802

gtc cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctg gag 850 Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu 210 215 220	
aca ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa cct 898 Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro 225 230 235 240	
aag gat aaa gac cct gaa caa ggc cac ttc ctc tgg att gcg gct gta 946 Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val 245 250 255	
ctt gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca cta 994 Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu 260 265 270	-
agg aaa agg aag aag cag cct ggc ccc tct cat gaa tgt gaa acc 1042 Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr 275 280 285	
atc aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta cca 1090 Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro 290 295 300	
tac cac gta cct gag aga tct gat gaa gcc cag tgt att aac att ttg 1138  Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu  305 310 315 320	
aag aca gcc tca ggc gac aaa agt act aca cat ttt taattaaaga 1184 Lys Thr Ala Ser Gly Asp Lys Ser Thr Thr His Phe 325 330	
ataaagtcca tataactgtc cattgtttat atgcctttcc cttcaagttt tgggcttacc 1244	
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<sup>&</sup>lt;210> 26

<sup>&</sup>lt;211> 332

<sup>&</sup>lt;212> PRT

<sup>&</sup>lt;213> Felis catus

<sup>&</sup>lt;400> 26

Met Gly Ile Cys Asp Ser Thr Met Gly Leu Ser His Thr Leu Leu Val 5 10 Met Ala Leu Leu Ser Gly Val Ser Ser Met Lys Ser Gln Ala Tyr Phe Asn Lys Thr Gly Glu Leu Pro Cys His Phe Thr Asn Ser Gln Asn 40 Ile Ser Leu Asp Glu Leu Val Val Phe Trp Gln Asp Gln Asp Lys Leu Val Leu Tyr Glu Ile Phe Arg Gly Lys Glu Asn Pro Gln Asn Val His 70 75 Leu Lys Tyr Lys Gly Arg Thr Ser Phe Asp Lys Asp Asn Trp Thr Leu 85 90 Arg Leu His Asn Val Gln Ile Lys Asp Lys Gly Thr Tyr His Cys Phe 100 . Ile His Tyr Lys Gly Pro Lys Gly Leu Val Pro Met His Gln Met Ser Ser Asp Leu Ser Val Leu Ala Asn Phe Ser Gln Pro Glu Ile Thr Val 135 Thr Ser Asn Arg Thr Glu Asn Ser Gly Ile Ile Asn Leu Thr Cys Ser 145 150 155 Ser Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn 165 170 Thr Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln 180 185 Asn Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser 200 Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu 210 215 220 Thr Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro 225 230 235 Lys Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val 245 250

Leu Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu 260 265 270

Arg Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr 275 280 285

Ile Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro 290 295 300

Tyr His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu 305 310 315 320

Lys Thr Ala Ser Gly Asp Lys Ser Thr Thr His Phe 325 330

<210> 27

<211> 2830

<212> DNA

<213> Felis catus

<400> 27

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tactgttatt tcaggttgac tgaagttagc aagcactgat aggtcagaac tcatttggtg 2280 catgggaact agtcctttgg gcccttata atgaatgaaa cagtgatatg tgcccttgtc 2340 cttgatctga acattgtgga gtctcagggt ccagttgtcc ttgtcaaagc ttgtacggcc 2400 cttatatttg agatgaacat tttgagggtt ctctttgcct ctgaatatct catacagaac 2460 cagcttatcc tggtcctgcc aaaatactac cagctcatcc aggcttatgt tttgagagtt 2520 tgtaaaatgg catggcagtt ctccagtctt gttgaaatat gcttgactct tcatggaaga 2580 aacaccagag agcaggagg ccatcacaag gagagtgtga ctcagtcca tagtgctgtc 2640 acaaatgccc atccactgca gctcccagag accagatgta taagctcagt gacattcccg 2700 aggaacacag aaacaaggtg ttaagaataa acgatgagga gcctttgtga gctccccata 2760 acttcctaac actcttgta gagaaagaaa taatgtcagg gctgagacta gaactcaaaa 2820 aaaaaaaaaac

<210> 28

<211> 996

<212> DNA

<213> Felis catus

<400> 28

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gtttctatca gcttgccttt ttcagtccct gaagcacaca atgtgagcgt cttttgtgcc 660 ctgaaactgg agacactgga gatgctgctc tccctacctt tcaatataga tgcacaacct 720 aaggataaag accctgaaca aggccacttc ctctggattg cggctgtact tgtaatgttt 780 gttgttttt gtgggatggt gtcctttaaa acactaagga aaaggaagaa gaagcagcct 840 ggcccctctc atgaatgtga aaccatcaaa agggagagaa aagagagcaa acagaccaac 900 gaaagagtac cataccacgt acctgagaga tctgatgaag cccagtgtat taacattttg 960 aagacagcct caggcgacaa aagtactaca catttt 996

<210> 29

<211> 996

<212> DNA

<213> Felis catus

<400> 29
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ctcccttttg atggtttcac attcatgaga ggggccaggc tgcttcttct tccttttcct 180
tagtgtttta aaggacacca tcccacaaaa aacaacaaac attacaagta cagccgcaat 240
ccagaggaag tggccttgtt cagggtcttt atccttaggt tgtgcatcta tattgaaagg 300
tagggagagc agcatctcca gtgtctccag tttcagggca caaaagacgc tcacattgtg 360
tgcttcaggg actgaaaaag gcaagctgat agaaacgttg tacagttctg tcacattatt 420
ttgagatttc ttcatgacag tatcatactt agtagttgaa ttctcagtgt ttagctgaaa 480
atacatctcc ttaggttctg ggtaaccttg tattgagtga caggtcaaat ttatgatgcc 540
agaattttct gttctattag aagttactgt tatttcaggt tgactgaagt tagcaagcac 600
tgataggtca gaactcattt ggtgcatggg aactagtcct ttgggccctt tataatgaat 660
gaaacagtga tatgtgccct tgtccttgat ctgaacattg tggagtctca gggtccagtt 720
gtccttgtca aagcttgtac ggcccttata tttgagatga acattttgag ggttctcttt 780

<210> 30 <211> 509 <212> DNA <213> Felis catus <220> <221> CDS <222> (1)..(507) <400> 30 ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta aac act Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 gag aat toa act act aag tat gat act gtc atg aag aaa tot caa aat 96 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 25 aat gtg aca gaa ctg tac aac gtt tct atc agc ttg cct ttt tca gtc Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctq qaq aca 192 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 50 55 ctg gag atg ctg ctc tcc cta cct ttc aat ata gat gca caa cct aaq Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 65 70 gat aaa gac cet gaa caa ggc cac tte etc tgg att geg get gta ett Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu 85 90 gta atg ttt gtt gtt ttt tgt ggg atg gtg tcc ttt aaa aca cta agg 336 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 100 105 110

aaa agg aag aag cag cct ggc ccc tct cat gaa tgt gaa acc atc

384

Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 125 120 115 aaa agg gag aga aaa gag agc aaa cag acc aac gaa aga gta cca tac 432 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr 135 130 cac qta cct gag aga tct gat gaa gcc cag tgt att aac att ttg aag His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys 155 145 150 aca gcc tca ggc gac aaa agt act aca ca 509 Thr Ala Ser Gly Asp Lys Ser Thr Thr 165 <210> 31 <211> 169 <212> PRT <213> Felis catus <400> 31 Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 5 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 25 20 Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 40 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 55 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Asp Ala Gln Pro Lys 70 65 Asp Lys Asp Pro Glu Gln Gly His Phe Leu Trp Ile Ala Ala Val Leu 90 85 Val Met Phe Val Val Phe Cys Gly Met Val Ser Phe Lys Thr Leu Arg 100 105 Lys Arg Lys Lys Gln Pro Gly Pro Ser His Glu Cys Glu Thr Ile 120 Lys Arg Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr 130 135

His Val Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys 145 150 155 160

Thr Ala Ser Gly Asp Lys Ser Thr Thr 165

<210> 32

<211> 509

<212> DNA

<213> Felis catus

<400> 32

tgtgtagtac ttttgtcgcc tgaggctgtc ttcaaaatgt taatacactg ggcttcatca 60

gatctctcag gtacgtggta tggtactctt tcgttggtct gtttgctctc ttttctccc 120

cttttgatgg tttcacattc atgagagggg ccaggctgct tcttcttcct tttccttagt 180

gttttaaagg acaccatccc acaaaaaaca acaaacatta caagtacagc cgcaatccag 240

aggaagtggc cttgttcagg gtctttatcc ttaggttgtg catctatatt gaaaggtagg 300

gagagcagca tctccagtgt ctccagtttc agggcacaaa agacgctcac attgtgtgct 360

tcagggactg aaaaaggcaa gctgatagaa acgttgtaca gttctgtcac attatttga 420

gatttcttca tgacagtatc atacttagta gttgaattct cagtgtttag ctgaaaatac 480

atctccttag gttctgggta accttgtat

<210> 33

<211> 359

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(357)

<400> 33

ata caa ggt tac cca gaa cct aag gag atg tat ttt cag cta aac act 48

Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr

1 5 10 15

gag aat toa act act aag tat gat act gtc atg aag aaa tot caa aat 96

Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 25 aat gtg aca gaa ctg tac aac gtt tct atc agc ttg cct ttt tca gtc Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val 35 40 cct gaa gca cac aat gtg agc gtc ttt tgt gcc ctg aaa ctg gag aca 192 Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 50 55 ctg gag atg ctg ctc tcc cta cct ttc aat ata gaa acc atc aaa agg Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Glu Thr Ile Lys Arg 65 70 75 gag aga aaa gag agc aaa cag acc aac gaa aga gta cca tac cac gta 288 Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr His Val 85 cct gag aga tct gat gaa gcc cag tgt att aac att ttg aag aca gcc 336 Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys Thr Ala 105 100 359 tca ggc gac aaa agt act aca ca Ser Gly Asp Lys Ser Thr Thr 115 <210> 34 <211> 119 <212> PRT <213> Felis catus <400> 34 Ile Gln Gly Tyr Pro Glu Pro Lys Glu Met Tyr Phe Gln Leu Asn Thr 10 5 Glu Asn Ser Thr Thr Lys Tyr Asp Thr Val Met Lys Lys Ser Gln Asn 20 . 25 Asn Val Thr Glu Leu Tyr Asn Val Ser Ile Ser Leu Pro Phe Ser Val Pro Glu Ala His Asn Val Ser Val Phe Cys Ala Leu Lys Leu Glu Thr 55 Leu Glu Met Leu Leu Ser Leu Pro Phe Asn Ile Glu Thr Ile Lys Arg 65 70

Glu Arg Lys Glu Ser Lys Gln Thr Asn Glu Arg Val Pro Tyr His Val 85 90 95

Pro Glu Arg Ser Asp Glu Ala Gln Cys Ile Asn Ile Leu Lys Thr Ala 100 105 110

Ser Gly Asp Lys Ser Thr Thr 115

<210> 35

<211> 359

<212> DNA

<213> Felis catus

<400> 35

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<210> 36

<211> 594

<212> DNA

<213> Felis catus

<220>

<221> CDS

<222> (1)..(522)

<400> 36

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Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Leu Lys His Pro Tyr
1 5 10 15

ccc aag ctc ttt ccg ctc ttg atg cta gct agt ctt ttt tac ttc tgt .96
Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
20 25 30

tca	ggt	atc	atc	cag	gtg	aac	aag	aca	gtg	gaa	gaa	gta	gca	gta	cta	144
Ser	Gly	Ile	Ile	Gln	Val	Asn	Lys	Thr	Val	Glu	Glu	Val	Ala	Val	Leu	
		35					40					45				
tcc	tgt	gat	.tac	aac	att	tcc	acc	aaa	gaa	ctg	acg	gaa	att	cga	atc	192
Ser	Cys	Asp	Tyr	Asn	Ile	Ser	Thr	Lys	Glu	Leu	Thr	Glu	Ile	Arg	Ile	
•	50					55					60					
tat	tgg	caa	aag	gat	gat	gaa	atg	gtg	ttg	gct	gtc	atg	tct	qqc	aaa	240
			Lys													
65	_		•	•	70					75				-	80	
gta	caa	ata	tgg	ccc	aaq	tac	aaq	aac	cqc	aca	ttc	act	gac	atc	acc	288
-			Trp		-		_		-				-	-		
				85		- 4			90					95		
gat	aac	cac	tcc	att	ata	atc	ato	act	cta	cac	cta	tca	σac	aat	aac	336
-			Ser				_	-	_		_		-			
			100					105					110		,	
				•												
aaa	tac	act	tgt	att	att	саа	ааσ	att	αаа	aaa	aaa	tet	tac	aaa	ata	384
			Cys													204
Ly S	1 y ±	115	Cys	116	110	01	120		010	<b></b> , 0	CLY	125	1 7 1	ny 3	Val	
		110					120					120				
aaa	cac	cta	act	tca	ata	atσ	tta	tta	atc	ада	aac	atc	aca	ccc	age	432
			Thr	_		_									_	102
<i>D</i> <b>y</b> <i>S</i>	130	LCu	1111	501	<b>v</b> a	135	200	۵۰۵	· u _	9	140	• • •	****	110	001	
	150			•		133					140					
aca	gag	CCC	aat	acc	cat	aca	gag	ctt	gaa	atc	atα	acc	cta	aαa	tca	480
			Asn	_		-	-						_	_		100
145	014		HOII	711.0	150		0.1.0	<b></b>	014	155	1100		Deu	2119	160	
143					130					133					100	
2012	cct	a a a	ctg	202	tca	242	atc	aaa	cac	tta	atc	asc.	tas			522
_			Leu	_									cya			322
ALG	PIO	GIU	Leu	165	Ser	Arg	vaı	GTĀ	170	пеп	116	ASP				
				163				•	170							
~~~	2025		<b></b>							a+ a+	+					E00
gcc	accc.	ayg	Catc	ccaa	rg a	Lacti	LLCT	a aa	Laddi	ulct	Lada	adādi	ada	aaadi	aaaaa	202
																E C 4
aaa	aaaa	aaa	aa													594

<210> 37

<211> 173

<212> PRT .

<213> Felis catus

<400> 37

Met Gly His Ala Ala Lys Trp Lys Thr Pro Leu Leu Lys His Pro Tyr

1 5 10 15

Pro Lys Leu Phe Pro Leu Leu Met Leu Ala Ser Leu Phe Tyr Phe Cys
20 25 30

Ser Gly Ile Ile Gln Val Asn Lys Thr Val Glu Glu Val Ala Val Leu 35 40 45

Ser Cys Asp Tyr Asn Ile Ser Thr Lys Glu Leu Thr Glu Ile Arg Ile 50 55 60

Tyr Trp Gln Lys Asp Asp Glu Met Val Leu Ala Val Met Ser Gly Lys 65 70 75 80

Val Gln Val Trp Pro Lys Tyr Lys Asn Arg Thr Phe Thr Asp Val Thr 85 90 95

Asp Asn His Ser Ile Val Ile Met Ala Leu Arg Leu Ser Asp Asn Gly
100 105 110

Lys Tyr Thr Cys Ile Ile Gln Lys Ile Glu Lys Gly Ser Tyr Lys Val 115 120 125

Lys His Leu Thr Ser Val Met Leu Leu Val Arg Gly Val Thr Pro Ser 130 135 140

Thr Glu Pro Asn Ala His Ala Glu Leu Glu Ile Met Thr Leu Arg Ser 145 150 155 160

Arg Pro Glu Leu Arg Ser Arg Val Gly Arg Leu Ile Asp 165 170

<210> 38

<211> 594

<212> DNA

<213> Felis catus

<400> 38

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agacatgaca gccaacacca tttcatcate ettttgccaa tagattegaa tttcegtcag 420
ttctttggtg gaaatgttgt aatcacagga tagtactget acttetteca etgtettgtt 480
cacetggatg atacetgaac agaagtaaaa aagactaget agcatcaaga geggaaagag 540
ettgggatat gggtgettea gtagtggtgt tttccacttt getgegtgac ecat 594

<210> 39

<211> 519

<212> DNA

<213> Felis catus

<400> 39

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<210> 40

<211> 519

<212> DNA

<213> Felis catus

<400> 40

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WO 99/47558 PCT/US99/0618<sup>-</sup>

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	gttgtaatca	cagga	tagta	ctgcta	cttc	ttc	cact	gtc	ttgt	tcac	ct g	gatg	atacc	420
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	tct agg ac Ser Arg Th													155
	gtc ttc to Val Phe Se													203
	agc agc co Ser Ser A				Phe									251
	aac gca g Asn Ala A 65													299
	atg act g Met Thr G													347

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														tac Tyr		443
_	_				_							-		atg Met		491
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_							-	-	_	_	_		_	ttt Phe 175		587
	-					-	_		-	_		_		aag Lys		635
-	_													act Thr		683
		Cys	gaa Glu											aat Asn	tga	731
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<210> 42

<211> 223

<212> PRT

<213> Canis familiaris

<400> 42

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Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Leu Ala 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly
50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Ala Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asp Glu Leu Ala 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Thr Ser Ser Gly Asn Lys Val

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Val Gly Met Gly 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 : 170 : 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 43

<211> 1856

<212> DNA

<213> Canis familiaris

<400> 43

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attaaccatg agcaaggaat tggggccctt gtgaaactag agcttccttg aagttcatac 240
ctccaagact cctggaatga gccgtttact tgacgatggt gttctatgga gttaaatcag 300
atataccagt tttgactccc ttacaaatct ttgaaaggag ctaacataaa agcccaaagc 360
acatgtcaac accaatttag cccaacagt ctacaagaat caactatgac ctcatccagt 420
ttccaagcca gttaccaagt gaccttgtat tttacctggc gtattagtgt cctgaatccc 480

tccataaaac ttcccctgag cccctggtgg gaagacactg ccatatagtg tttatattga 540 aaccatcaac aaatacacaa aagcacatgt ggcccccatg cataatacta tcagataaaa 600 aaatatatat tggtacaata caacctttgg aatcactggc taaaatatag ccatgtgaat 660 atttttaaag tcttcacgtg attttacatt tatgaaaaat aacatagcac aaaaatttaa 720 cttgaaaacg tcacttcagc tataaacttc tcacatgtaa atacaaagtg tgtacaatat 780 catectetee etgactetet etcetttget ttetttggae egeaceaete ectaacetat 840 atcctagage geatgteeta atgctgeate eccatattge teccaagtga tacttttaeg 900 aaaattggat ctgatgtgac agaaacatcc tggctctgtt ttcttgcacc tttgctttqa 960 atttgtagta cacttcattt gggttctgca tccagcttta tattaaagag agatgaaacc 1020 cccccaaaa tatacaaaca agtacacata gctggatagc acaaagttag aattgcctca 1080 gctcctggaa attggaaaat attctttctt cttcataatg atctctcaat tgatgggaat 1140 aaaataaggc tgaaattgct tttcacattc tggctcagtt gggggcattt tcacatagac 1200 ccctgtggta agagggcttc ttttctttag cattttgctc aaagaaacag ctgtgataag 1260 aaagctataa aaaaacaagc ccgaactgac tgctgcaagg atccagagga ggaagtcaga 1320 atctgggcaa ggttcaggat cgatgacata aatctgggtt ccatttccca tgcctacata 1380 gtagggtggt gggtacatga gctccacctt gcagatgtag agccccqtqt ccatqqccct 1440 caaccettgg atggtgaggt teactttgtt tecaetggag gtgeeggtge aggtagaate 1500 atccaggaag gccaactcat cctccactgt gtatgtcgcg gcacagactt cagtcatctg 1560 gctgccagcc tgccgcagca ctgtcacccg gacctcggct gcgttgcctg aagacccata 1620 ttcacacacg aagctagcaa cacccegget getggecaga accaetgeag getgagecae 1680 ggtcctagaa gccaggtccg gctgagcccc atgcctccgg aatccaaagc cagccatggc 1800 tttatggagc agtgttcagg tcttcaggaa gcagagtgaa acctttcagg atcctg 1856

<210> 44

<211> 669

<212> DNA

<213> Canis familiaris

<400> 44

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<210> 45

<211> 669

<212> DNA

<213> Canis familiaris

<400> 45

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ttteacatag acceetgtgg taagaggget tettttettt ageattttge teaaagaaac 120

agetgtgata agaaagetat aaaaaaacaa geeegaactg aetgetgeaa ggateeagag 180

gaggaagtea gaatetggge aaggtteagg ategatgaca taaatetggg tteeatttee 240

catgeetaca tagtagggtg gtgggtacat gageteeace ttgeagatgt agageeeegt 300

gteeatggee eteaaeeett ggatggtgag gtteaeetttg ttteeaetgg aggtgeeggt 360

<210> 46 <211> 1883 <212> DNA

<213> Felis catus

<220>
<221> CDS
<222> (69)..(740)

<400> 46

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ataaagcc atg gct tgc ttt gga ttc cgg agg cat ggg gct cag ctg gac 110

Met Ala Cys Phe Gly Phe Arg Arg His Gly Ala Gln Leu Asp

1 5 10

ctg gct tct agg acc tgg ccc tgc act gct ctg ttt tct ctt ctc ttt 158
Leu Ala Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe
15 20 25 30

atc ccc gtc ttc tcc aaa ggg atg cat gtg gcc cag cct gca gtg gtg 206 .

Ile Pro Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val
35 40 45

ctg gcc agc cga ggt gtc gcc agc ttc gtg tgt gaa tat ggg tct 254 Leu Ala Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser 50 55 60

tca ggc aat gcc gcc gaa gtc cga gtg act gtg ctg agg cag act ggc 302 Ser Gly Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly 65 70 75

age cag atg act gaa gte tgt get geg aca tac aca gtg gag aat gag 350 Ser Gln Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu 80 85 90

-	-			-	-			tgc Cys					•			398
								ttg Leu								446
								tac Tyr 135								494 ·
_			-		_			gtc Val								542
_		-						ctc Leu	_	_	_	-			-	590
								gct Ala								638
								GJ À aaa								686
								ttt Phe 215								734
aat Asn		cac	accg	tta '	tgaa	gaag ·	ga a	gaac	actg	t cca	aatt	tcta	aga	gctga	agg	790
caa	ttct	aac	tttt	tgct	at c	cagc	tatg	t tg	ctta	tttg	tgt	attt <sup>.</sup>	tgg	gggg	ggattc	850
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															gggtta	
															ttgtac	
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aaaaaaaaaa aaa 1870
aaaaaaaaaa aaa

<210> 47

<211> 223

<212> PRT

<213> Felis catus

<400> 47

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1 5 10 15

Ser Arg Thr Trp Pro Cys Thr Ala Leu Phe Ser Leu Leu Phe Ile Pro 20 25 30

Val Phe Ser Lys Gly Met His Val Ala Gln Pro Ala Val Val Leu Ala . 35 40 45

Ser Ser Arg Gly Val Ala Ser Phe Val Cys Glu Tyr Gly Ser Ser Gly
50 55 60

Asn Ala Ala Glu Val Arg Val Thr Val Leu Arg Gln Thr Gly Ser Gln 65 70 75 80

Met Thr Glu Val Cys Ala Ala Thr Tyr Thr Val Glu Asn Glu Leu Ala 85 90 95

Phe Leu Asp Asp Ser Thr Cys Thr Gly Ile Ser Ser Gly Asn Lys Val

Asn Leu Thr Ile Gln Gly Leu Arg Ala Met Asp Thr Gly Leu Tyr Ile 115 120 125

Cys Lys Val Glu Leu Met Tyr Pro Pro Pro Tyr Tyr Ala Gly Met Gly 130 135 140

Asn Gly Thr Gln Ile Tyr Val Ile Asp Pro Glu Pro Cys Pro Asp Ser 145 150 155 160

Asp Phe Leu Leu Trp Ile Leu Ala Ala Val Ser Ser Gly Leu Phe Phe 165 170 175

Tyr Ser Phe Leu Ile Thr Ala Val Ser Leu Ser Lys Met Leu Lys Lys 180 185 190

Arg Ser Pro Leu Thr Thr Gly Val Tyr Val Lys Met Pro Pro Thr Glu 195 200 205

Pro Glu Cys Glu Lys Gln Phe Gln Pro Tyr Phe Ile Pro Ile Asn 210 215 220

<210> 48

<211> 1883

<212> DNA

<213> Felis catus

<400> 48

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1883

<210> 49 <211> 669

<212> DNA

<213> Felis catus

<400> 49

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<210> 50

<211> 669

<212> DNA

<213> Felis catus

<400> 50

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<213> Artificial Sequence

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<210> 57

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<b>\</b> 2237	Description of Artificial Sequence: Primer	Synthetic	
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<b>-210</b> >	50		
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	Artificial Sequence		
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90000	·		
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	> 28 > DNA > Artificial Sequence	·
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PCT/US99/06187

Primer Primer	,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,
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